

EXHIBIT A

Paper copy of Sequence Listings filed in
U.S. Provisional Application 60/155,241
(Attorney Docket No. PF-0557 US)

PF-0557 US

SEQUENCE LISTING

<110> Bandman, Olga
 Hillman, Jennifer L.
 Gorgone, Gina
 Guegler, Karl J.
 Corley, Neil C.
 Baughn, Mariah R.

<120> HUMAN CYTOCHROMES

<130> PF-0557 US

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 444

<212> PRT

<213> HOMO SAPIENS

<220>

<223> 008879, HMC1NOT01

<400> 1

Met	Gly	Lys	Gly	Gly	Asn	Gln	Gly	Glu	Gly	Ala	Ala	Glu	Arg	Glu	Val
1			5					10						15	
Ser	Val	Pro	Thr	Phe	Ser	Trp	Glu	Glu	Ile	Gln	Lys	His	Asn	Leu	Arg
			20				25					30			
Thr	Asp	Ser	Gly	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	Ile	Thr	Lys
		35					40					45			
Trp	Ser	Ile	Gln	His	Pro	Gly	Gly	Gln	Arg	Val	Ile	Gly	His	Tyr	Ala
	50				55					60					
Gly	Glu	Asp	Ala	Thr	Asp	Ala	Phe	Arg	Ala	Phe	His	Pro	Asp	Leu	Glu
65				70					75					80	
Phe	Val	Gly	Lys	Phe	Leu	Lys	Pro	Leu	Leu	Ile	Gly	Glu	Leu	Ala	Pro
			85					90						95	
Glu	Glu	Pro	Ser	Gln	Asp	His	Gly	Lys	Asn	Ser	Lys	Ile	Thr	Glu	Asp
			100				105						110		
Phe	Arg	Ala	Leu	Arg	Lys	Thr	Ala	Glu	Asp	Met	Asn	Leu	Phe	Lys	Thr
		115				120						125			
Asn	His	Val	Phe	Phe	Leu	Leu	Leu	Ala	His	Ile	Ile	Ala	Leu	Glu	
	130				135					140					
Ser	Ile	Ala	Trp	Phe	Thr	Val	Phe	Tyr	Phe	Gly	Asn	Gly	Trp	Ile	Pro
145				150					155					160	
Thr	Leu	Ile	Thr	Ala	Phe	Val	Leu	Ala	Thr	Ser	Gln	Ala	Gln	Ala	Gly
			165					170						175	
Trp	Leu	Gln	His	Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	Arg	Lys	Pro	Lys
		180				185							190		
Trp	Asn	His	Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala
		195				200						205			
Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	His	Ala	Lys	Pro
	210				215					220					
Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	Val	Phe	Val
225				230					235					240	
Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	Tyr
			245					250					255		
Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro
		260					265						270		
Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	Ile	Ile	Met	Thr	Met	Ile
		275					280					285			
Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	Trp	Ala	Val	Ser	Tyr	Tyr	Ile
	290					295				300					
Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu

PF-0557 US

```

305          310          315          320
Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp
          325          330          335
Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr
          340          345          350
Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
          355          360          365
Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
          370          375          380
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala
385          390          395          400
Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu
          405          410          415
Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys
          420          425          430
Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
          435          440

```

```

<210> 2
<211> 286
<212> PRT
<213> HOMO SAPIENS

```

```

<220>
<223> 2274011, PROSNON01

```

```

<400> 2
Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Ala Leu Leu Gly Ser Ala
1          5          10          15
Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
          20          25          30
His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
          35          40          45
Trp His Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile
          50          55          60
Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
65          70          75          80
Leu Met Lys Ser Ile His Ala Gly Leu Asn Ala Val Ala Ala Ile Leu
          85          90          95
Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn
          100          105          110
Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala Val
          115          120          125
Ile Cys Tyr Leu Leu Gln Leu Leu Ser Gly Phe Ser Val Phe Leu Leu
          130          135          140
Pro Trp Ala Pro Leu Ser Leu Arg Ala Phe Leu Met Pro Ile His Val
145          150          155          160
Tyr Ser Gly Ile Val Ile Phe Gly Thr Val Ile Ala Thr Ala Leu Met
          165          170          175
Gly Leu Thr Glu Lys Leu Ile Phe Ser Leu Arg Asp Pro Ala Tyr Ser
          180          185          190
Thr Phe Pro Pro Glu Gly Val Phe Val Asn Thr Leu Gly Leu Leu Ile
          195          200          205
Leu Val Phe Gly Ala Leu Ile Phe Trp Ile Val Thr Arg Pro Gln Trp
          210          215          220
Lys Arg Pro Lys Glu Pro Asn Ser Thr Ile Leu His Pro Asn Gly Gly
225          230          235          240
Thr Glu Gln Gly Ala Arg Gly Ser Met Pro Ala Tyr Ser Gly Asn Asn
          245          250          255
Met Asp Lys Ser Asp Ser Glu Leu Asn Asn Glu Val Ala Ala Arg Lys
          260          265          270
Arg Asn Leu Ala Leu Asp Glu Ala Gly Gln Arg Ser Thr Met
          275          280          285

```

```

<210> 3
<211> 3184
<212> DNA

```

PF-0557 US

<213> HOMO SAPIENS

<220>

<223> 008879, HMC1NOT01

<400> 3

ctccccgagcg	caggcgagag	ggctggggga	ggggggcgcg	tgggaggagt	aggagaagac	60
aaaagccgaa	agcgaagagg	gccggggctg	cacacaccgg	ctgggaggca	gccgtctgtg	120
cagcgagcag	ccggcgcggg	gaggccgcag	tgcacggggc	gtcacagtcg	gcaggcagca	180
tgggggaagg	agggaaaccag	ggcgaggggg	ccggccgagcg	cgaggtgtcg	gtgcccacct	240
tcagctggga	ggagattcag	aagcataacc	tgcgcaccga	cagtgggctg	gtcattgacc	300
gcaaggttta	caacatcacc	aaatgggtcca	tccagcaccg	ggggggccag	cggttcacog	360
ggcactacgc	tggagaagat	gcaacgggatg	ccttcgcgcg	cttcaccctt	gacctggaat	420
tctgtgggcaa	gttcttgaaa	cccctgtctga	ttggtgaact	ggccccggag	gagcccagcc	480
aggaccacgg	caagaactca	aagatcactg	aggacttcgg	ggccctgagg	aagacggctg	540
aggacatgaa	cctgttcaag	accaaccacg	tgttcttctt	cctctctctg	gcccacatca	600
tgcacctgga	gagcattgca	tggttcactg	tcttctactt	tggcaatggc	tggattccta	660
ccctcatcac	ggcctttgtc	cttgcctacct	ctcaggccca	agctggatgg	ctgcaacatg	720
attatggcca	cctgtctgtc	tacagaaaac	ccaagtggaa	ccacctgtgc	cacaaattcg	780
tcattggcca	cttaaagggt	gcctctgcca	actggtggaa	tcacgcgcac	ttccagcacc	840
acgccaagcc	taacatcttc	cacaaggatc	ccgatgtgaa	catgctgcac	gtgtttgttc	900
tgggccaagt	gcagcccac	gagtacggca	agagaagact	gaaatactcg	ccctacaatc	960
accagcacga	atacttcttc	ctgattgggc	cgccgctgct	catccccatg	tatttccagt	1020
accagatcat	catgaccatg	atcgctccata	agaactgggt	ggacctggcc	tgggcccgtca	1080
gctactacat	ccggttcttc	atcacctaca	tcccttctta	cgccatccctg	ggagccctcc	1140
tttctctcaa	cttcatcagg	ttcctggaga	gccactgggt	tgtgtgggtc	acacagatga	1200
atcacatcgt	catggagatt	gaccaggagg	cctaccgtga	ctggttcagt	agccagctga	1260
cagccacctg	caacgtggag	cagtccttct	tcaacgactg	gttcagtggg	caccttaact	1320
tccagattga	gcaccacctc	ttcccaccga	tgcctccggca	caacttacac	aagatcgccc	1380
cgctgggtgaa	gtctctatgt	gccaagcatg	gcattgaata	ccaggagaag	ccgctactga	1440
ggggccctgct	ggacatcatc	agggtccctga	agaagtctgg	gaagctgtgg	ctggaccgct	1500
accttcacaa	atgaagccac	agccccgggg	acaccgtggg	gaagggggtc	agggtgggtg	1560
atggccagag	gaatgatggg	cttttgttct	gaggggtgtc	cgagaggctg	gtgtatgcac	1620
tgtctacgga	ccccatgttg	gatctttctc	cctttctctt	ctcctttttc	tcttcacatc	1680
tcccccatag	caccctgccc	tcatgggacc	tgcctccctt	cagccgtcag	ccatcagcca	1740
tggccctccc	agtgcctctt	agcccttctt	tcaaaggagc	agagagggtg	ccaccggggg	1800
tggctctgtc	ctacctccac	tctctgcccc	taaagatggg	aggagaccag	cggctccatgg	1860
gtctggccctg	tgagtctccc	cttgccagcct	ggctcactagg	catcaccccc	gctttgggtc	1920
ttcagatgct	cttgggggtc	ataggggagc	gtcctagtgc	ggcagggccc	ctgacctctc	1980
cggccctggct	tcaactctcc	tgcaggctgc	cattgggtcca	cctttctata	gagaggcctg	2040
ctttgttaca	aagctcgggt	ctccctcctg	cagctcgggt	aagtaaccga	ggctctctct	2100
aagatgtcca	ggggcccagg	cccgccggga	cagccagccc	aaaccttggg	ccctggaaga	2160
gtctccacc	ccatcactag	agtgtctctga	ccctgggctt	tcacggggcc	cattccaccg	2220
cctccccaac	ttgagcctgt	gaccttggga	ccaaaggggg	agtccctcgt	ctcttgtgac	2280
tcagcagagg	cagtggccac	gttcaggagg	gggcccggctg	gcctggaggc	tcagcccacc	2340
ctccagcttt	tctcagggtt	gtcctgaggt	ccaagattct	ggagcaatct	gaccttctc	2400
caaaggctct	gttctcagct	gggcagtgc	agccaatccc	tggccatttg	gccccagggg	2460
gacgtggggc	ctgcaggctg	caggagggca	ctggagctgg	gaggtctcgt	cccagccctc	2520
cccactctcg	ggctgctgtg	tggacggcgc	tgcctcaggc	actctcctgt	ctgaacctgc	2580
ccttactgtg	tttaacctgt	tgtctccagg	tgcattctga	taggaggggg	cggcaggggt	2640
gggccttgtg	acaactgtgc	tttcaccaca	tggccttgc	tcgggtggcc	tgaotgtcag	2700
ggagggccag	ggaggcagag	cgggaggggg	tctcaggagg	aggctgccc	gaggggctgg	2760
ggagggggta	cctcatgagg	accagggtgg	agctgagaag	aggaggagggt	gggggctgga	2820
ggtgctggta	gctgagggga	cgggcaagtg	agaggggagg	gaggggaagtc	ctgggaggat	2880
cctgagctgc	tgttgcagtc	taaccacta	atcagttctt	agattcaggg	gaagggcagg	2940
caccaacaac	tcagaatggg	ggctttcggg	gagggcgcc	agtcctccca	gctctaagca	3000
gccaggaggg	aootgcattc	aagcatctgg	gttgccatgg	caatggcatg	ccccccagct	3060
actgtatgcc	cccgaccccc	gcagaggcag	aatgaaccca	tagggagctg	atcgtaattg	3120
ttatcatgtt	acttccccac	ccctacattt	tttgaaataa	aataagggaat	tttaaaaaaa	3180
aaaa						3184

<210> 4

<211> 4298

<212> DNA

<213> HOMO SAPIENS

<220>

PF-0557 US

<223> 2274011, PROSNON01

<400> 4

cgcaggcgga	gacagcccca	agaagtcgac	gcctcggtcc	cgccgcccgg	ccactaccca	60
gagggtctgc	gccgcctctc	caagttcttg	tggcccccgc	ggtgcggagt	atggggcgct	120
gatggccatg	gagggtctact	ggcgcttctt	ggcgctgctg	gggtcggcac	tgctcgctcg	180
cttctgtctg	gtgatcttcg	cctcgctctg	ggctcctccac	taccgagagg	ggcttggctg	240
ggatgggagc	gcactagagt	ttaactggca	ccagtgcttc	atggtcaccg	gcttctgtct	300
catccagggc	atcgccatca	tcgtctacag	actgcccgtg	acctggaaat	gcagcaagct	360
cctgatgaaa	tccatccatg	caggggttaa	tgccagtgtg	gccattcttg	caattatctc	420
tgtggtggcc	gtgtttgaga	accacaatgt	taacaatata	gccaatatgt	acagtcctgca	480
cagctgggtt	ggactgatag	ctgtcatatg	ctatttgtta	cagcttcttt	cagggttttct	540
agtctttctg	cttccatggg	ctccgctttc	tctccgagca	tttctcatgc	ccatacatgt	600
ttattcttga	attgtcatct	ttggaacagt	gattgcaaca	gcacttatgg	gattgacaga	660
gaaactgatt	ttttccctga	gagatccctg	atacagtaaa	ttcccgccag	aagggtgtttt	720
cgtaaatatc	cttggccctc	tgatccctgg	gttcggggcc	ctcatttttt	ggatagtcac	780
cagaccgcaa	tggaacagtc	ctaaggagcc	aaattctacc	attcttcttc	caaatggagg	840
cactgaacag	ggagcaagag	gttccatgcc	agctactact	ggcaacaaca	tggacaaatc	900
agattcagag	ttaaacaatg	aagtagcagc	aaggaaaaga	aacttagctc	tggatgaggg	960
tgggcagaga	tctaccatgt	aaaatgttgt	agagatagag	ccatataaag	tcacgtttca	1020
aaactagctc	tacagttttg	cttctctctt	tagccatag	ataattgggc	tatgtagtat	1080
caatattttac	tttaatcaca	aaggatgggt	tcttgaaata	atttgtattg	attgaggcct	1140
atgaactgac	ctgaattgga	aaggatgtga	ttaatataaa	taatagcaga	tataaattgt	1200
ggtratgtta	ccttttatctt	gttgaggacc	acaacattag	cacgggtgct	tgtgcagaat	1260
agatactcaa	tatgtgaata	tgtgtctact	agtagttaat	tggataaaact	ggcagcatcc	1320
ctggcctgtt	gtcatgcagt	catttctctg	baattctggg	agacaatgat	ttcacaacta	1380
gaggggaagc	gtcctaaaaa	tttaaaatcc	gataaggaat	atctggggaca	gggttttagat	1440
catgactcta	cacagatacc	atgatgagag	tatatataag	aaatttagga	aagcacctgg	1500
ttcctttctc	cccagctctg	ccttctgctc	ctctcccagc	tgggtttggg	tcaaatgtgc	1560
cctggagaot	aggggtttatg	ttagggtatt	gatagattag	agcaggtggg	tgaagagatc	1620
ttctctggto	agacttggaa	gaatttccaa	aaactgaagt	agccccaaga	cttccctagg	1680
gttgatgtac	tttatgatcc	agatgctaaa	cttcttagat	tgaataatag	cttcaacact	1740
taagtagcat	acactgcctc	acaaacctca	gagagcactt	ttccccaagt	tcttgttttt	1800
atttttgaaa	gtactcacac	agcacttaact	atgctccaaa	cactcctcta	agcactttac	1860
acatatttag	tcatctagtc	cccagacaga	cgggatgaag	taggtattgt	tactgttccc	1920
atttttacag	tgagagattt	gaagcctggg	gaagctagta	actcaoccca	aggtoacacg	1980
gctcatatct	gggtgggactg	agaotcagat	gcaggcagtc	tggcacctca	gtctggattc	2040
taaccatttc	actaagctat	ttttgtcttg	tactactttg	acccacccct	gaataaacct	2100
caattgcttg	agtggggtgt	agttattaaa	gggatgcttt	ttacottttg	ctgtttgctg	2160
tggcagatcc	cccagataac	caaggaaaag	gggccaccca	tacottggaa	tagggcatag	2220
ggccctcaot	actgcccaaa	agccatggcc	tacottgaca	cttgtttgat	ottaaaattg	2280
tgtcttggta	acaaaagatt	tggacaggca	tactctgtag	tttcaagtta	attaattgca	2340
atatattttt	cttcaggatt	ttagctgctg	aaacaacttc	agtttggagc	taaaagagac	2400
ctgtctcatg	gtctgcccct	ccctggggca	atagctaggg	tcttctctga	tttttatgga	2460
attttagggg	atattttgag	ctttgggttc	tcagttagtg	attgagactt	ggaggtgact	2520
tttcatgttt	ggagtatcat	ctctgtcttg	gatctgggct	gacaaattaa	aaccttagagt	2580
agtgcctatg	ctgaatgat	acttttccatt	ttttgtttga	tttttttgcc	ttcccttcaa	2640
ttttaaactg	aagcattttt	atgtgggtag	aaactctaca	ccaaatacac	taaacatttt	2700
gggtgcttag	ggatttctct	ttaggtaact	ggtacttaact	tccaaagact	gaatacaagc	2760
cacactccat	catatccctt	aaacttcatg	aaaaaacatt	caagatcccc	ttgctgcaac	2820
actgttctct	tcttctctac	taaatcttat	ttccaaaatt	ggtaatatag	ccagaaggat	2880
ccccagtaac	cagccctctg	cctggcacaa	agtggtagca	caattaaatt	cagtatgggt	2940
ggagcatggt	acagtcttgg	tgccatagaa	ggagttagtg	catagtcaca	catcatttga	3000
taagttggat	gttccattac	atagagggaac	acaaaattcc	aggggttttg	gaggaaggga	3060
ttagatagtg	actaagcogc	cagaattggag	gtggccattc	ctttttgtat	aggctaagaa	3120
acaggttatc	agtgaanaag	taattatggc	tttggcacta	gaatagcact	gttgcaaggt	3180
attttaagca	cccocactct	agccctttat	tttatctttc	atgtgggcta	atgtgaggat	3240
aatcttacag	atattatagg	aatttctttt	ctatctttat	gaaaacaacg	tatacaaat	3300
atatctagaa	aacctttgtt	tgagactctt	atttaattgg	cttttgattc	taatgataat	3360
tgtacottta	tctttcaaaa	gotgatattt	octacctaag	catctcccga	gaaaaatato	3420
tcattaaaaa	gcccataaat	aatagggggg	aagaaaagct	taggtatcaa	ttccaaaaca	3480
gtgattgaaa	tttcccaaaa	taattatggo	tctgtgtcat	tccagagata	atctggcttg	3540
gtttacccca	taacttaatt	tcagaaaaga	aagctttatt	ttaacactca	tctgaatcaa	3600
cattaaagcc	ttttctctca	aagcgtttat	tgagaaactc	aatgaatat	actttttgaa	3660
ttactgtcat	caaaagtgtg	cggcttctct	tgtgtctgtg	gtcaaatgga	acotgccttc	3720
taagacattt	cttttctctt	acttgcattg	ttcatgttaa	gctgtgctgt	ttagaacaaa	3780
catctcagac	tttacaagaa	aatgacaaag	aaggcaattg	cactttttta	gggatatcga	3840

PF-0557 US

```

caagcagttt ctgttttcta aaggacaaaa tacagagtgt gtgtcatttt taattagatt 3900
ctttcccttg ctgagttgga aattccagtg cagcactgat tgaccacagt tgccaatcta 3960
aaagcacaaa gacagaagta aagctttatg ctaattttat ttcaatatga tagaaaattt 4020
atcttggtat gtcttttttt agataactcc agcaggaaac tgtaactgct atgtcttttag 4080
gaaaatgtag aagaaagaac attattattc ttttaattcct acaagggtact cgaaaacett 4140
aagtgaaaaa gattttctatc tttttatcct agcgcatctta tggaaaaaat attaatctac 4200
ctgaatattt tataattttg taggaaaaat atgcattctat tttttcttga cttcttttat 4260
atagtaataa aagttatttt ggaagctcaa aaaaaaaa 4298

```

<210> 5
 <211> 458
 <212> PRT
 <213> HELIANTHUS ANNUUS

<220>
 <223> 1040729, GenBank

<400> 5

Met	Val	Ser	Pro	Ser	Ile	Glu	Val	Leu	Asn	Ser	Ile	Ala	Asp	Gly	Lys
1				5					10					15	
Lys	Tyr	Ile	Thr	Ser	Lys	Glu	Leu	Lys	Lys	His	Asn	Asn	Pro	Asn	Asp
			20					25					30		
Leu	Trp	Ile	Ser	Ile	Leu	Gly	Lys	Val	Tyr	Asn	Val	Thr	Glu	Trp	Ala
			35				40					45			
Lys	Glu	His	Pro	Gly	Gly	Asp	Ala	Pro	Leu	Ile	Asn	Leu	Ala	Gly	Gln
			50			55					60				
Asp	Val	Thr	Asp	Ala	Phe	Ile	Ala	Phe	His	Pro	Gly	Thr	Ala	Trp	Lys
65					70				75					80	
His	Leu	Asp	Lys	Leu	Phe	Thr	Gly	Tyr	His	Leu	Lys	Asp	Tyr	Gln	Val
			85					90						95	
Ser	Asp	Ile	Ser	Arg	Asp	Tyr	Arg	Lys	Leu	Ala	Ser	Glu	Phe	Ala	Lys
			100					105					110		
Ala	Gly	Met	Phe	Glu	Lys	Lys	Gly	His	Gly	Val	Ile	Tyr	Ser	Leu	Cys
			115				120					125			
Phe	Val	Ser	Leu	Leu	Leu	Ser	Ala	Cys	Val	Tyr	Gly	Val	Leu	Tyr	Ser
			130				135				140				
Gly	Ser	Phe	Trp	Ile	His	Met	Leu	Ser	Gly	Ala	Ile	Leu	Gly	Leu	Ala
145					150				155					160	
Trp	Met	Gln	Ile	Ala	Tyr	Leu	Gly	His	Asp	Ala	Gly	His	Tyr	Gln	Met
			165					170						175	
Met	Ala	Thr	Arg	Gly	Trp	Asn	Lys	Phe	Ala	Gly	Ile	Phe	Ile	Gly	Asn
			180					185					190		
Cys	Ile	Thr	Gly	Ile	Ser	Ile	Ala	Trp	Trp	Lys	Trp	Thr	His	Asn	Ala
			195				200					205			
His	His	Ile	Ala	Cys	Asn	Ser	Leu	Asp	Tyr	Asp	Pro	Asp	Leu	Gln	His
			210				215				220				
Leu	Pro	Met	Leu	Ala	Val	Ser	Ser	Lys	Leu	Phe	Asn	Ser	Ile	Thr	Ser
225					230					235				240	
Val	Phe	Tyr	Gly	Arg	Gln	Leu	Thr	Phe	Asp	Pro	Leu	Ala	Arg	Phe	Phe
			245					250						255	
Val	Ser	Tyr	Gln	His	Tyr	Leu	Tyr	Tyr	Pro	Ile	Met	Cys	Val	Ala	Arg
			260					265					270		
Val	Asn	Leu	Tyr	Leu	Gln	Thr	Ile	Leu	Leu	Leu	Ile	Ser	Lys	Arg	Lys
			275				280					285			
Ile	Pro	Asp	Arg	Gly	Leu	Asn	Ile	Leu	Gly	Thr	Leu	Ile	Phe	Trp	Thr
			290				295				300				
Trp	Phe	Pro	Leu	Leu	Val	Ser	Arg	Leu	Pro	Asn	Trp	Pro	Glu	Arg	Val
305					310					315				320	
Ala	Phe	Val	Leu	Val	Ser	Phe	Cys	Val	Thr	Gly	Ile	Gln	His	Ile	Gln
			325					330						335	
Phe	Thr	Leu	Asn	His	Phe	Ser	Gly	Asp	Val	Tyr	Val	Gly	Pro	Pro	Lys
			340					345					350		
Gly	Asp	Asn	Trp	Phe	Glu	Lys	Gln	Thr	Arg	Gly	Thr	Ile	Asp	Ile	Ala
			355				360					365			
Cys	Ser	Ser	Trp	Met	Asp	Trp	Phe	Phe	Gly	Gly	Leu	Gln	Phe	Gln	Leu
			370				375				380				

PF-0557 US

Glu His His Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Ser Ile
 385 390 395 400
 Ser Pro Ile Cys Arg Glu Leu Cys Lys Lys Tyr Asn Leu Pro Tyr Val
 405 410 415
 Ser Leu Ser Phe Tyr Asp Ala Asn Val Thr Thr Leu Lys Thr Leu Arg
 420 425 430
 Thr Ala Ala Leu Gln Ala Arg Asp Leu Thr Asn Pro Ala Pro Gln Asn
 435 440 445
 Leu Ala Trp Glu Ala Phe Asn Thr His Gly
 450 455

<210> 6
 <211> 251
 <212> PRT
 <213> HOMO SAPIENS

<220>
 <223> 1345640, GenBank

<400> 6
 Met Glu Gly Gly Ala Ala Ala Thr Pro Thr Ala Leu Pro Tyr Tyr
 1 5 10 15
 Val Ala Phe Ser Gln Leu Leu Gly Leu Thr Leu Val Ala Met Thr Gly
 20 25 30
 Ala Trp Leu Gly Leu Tyr Arg Gly Ile Ala Trp Glu Ser Asp Leu
 35 40 45
 Gln Phe Asn Ala His Pro Leu Cys Met Val Ile Gly Leu Ile Phe Leu
 50 55 60
 Gln Gly Asn Ala Leu Leu Val Tyr Arg Val Phe Arg Asn Glu Ala Lys
 65 70 75 80
 Arg Thr Thr Lys Val Leu His Gly Leu Leu His Ile Phe Ala Leu Val
 85 90 95
 Ile Ala Leu Val Gly Leu Val Ala Val Phe Asp Tyr His Arg Lys Lys
 100 105 110
 Gly Tyr Ala Asp Leu Tyr Ser Leu His Ser Trp Cys Gly Ile Leu Val
 115 120 125
 Phe Val Leu Tyr Phe Val Gln Trp Leu Val Gly Phe Ser Phe Phe Leu
 130 135 140
 Phe Pro Gly Ala Ser Phe Ser Leu Arg Ser Arg Tyr Arg Pro Gln His
 145 150 155 160
 Ile Phe Phe Gly Ala Thr Ile Phe Leu Leu Pro Val Gly Thr Ala Leu
 165 170 175
 Leu Gly Leu Lys Glu Ala Leu Leu Phe Asn Leu Gly Gly Lys Tyr Ser
 180 185 190
 Ala Phe Glu Pro Glu Gly Val Leu Ala Asn Val Leu Gly Leu Leu Leu
 195 200 205
 Ala Cys Phe Gly Gly Ala Val Leu Tyr Ile Leu Thr Arg Ala Asp Trp
 210 215 220
 Lys Arg Pro Ser Gln Ala Glu Glu Gln Ala Leu Ser Met Asp Phe Lys
 225 230 235 240
 Thr Leu Arg Gln Gly Asp Ser Pro Gly Ser Gln
 245 250